

RESULT 2

S74981

glucose dehydrogenase-B - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein slr1608

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S74981

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N
DNA Res. 3, 109-136, 1996A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocyst*

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S74981

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-412

A;Cross-references: UNIPROT:P73001; UNIPARC:UPI000013AF0F; EMBL:D90902; GB:AB001339; N

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: gdhB

C;Superfamily: hypothetical protein b0837

Query Match 14.9%; Score 362; DB 1; Length 412;
 Best Local Similarity 26.3%; Pred. No. 1.5e-17;
 Matches 120; Conservative 63; Mismatches 175; Indels 98; Gaps 16;

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Qy      3 PLTPSQFAKAKSENFDDKKVILSNLNKPHALLWGPDNQIWLTER-ATGKILR---VNPES- 57
      | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      42 PTNSVEIVQANQPEIKAVPVIDGLEHPWGMALPNGDILITERPGRRLRIVRDGVLDPEAI 101

Qy      58 GSVKTVFQVPEIVNDADGQNGLLGFAPDFKNNPYIYISGTFKNPKSTDKELPNQTIIR 117
      | | | | | | | | | | | | | | | | : : | : | : | : | : | : | :
Db     102 AGVAVASTVSAQQLFASQQGGLLDIALHPRFAENRFVYFT-----YSHGTQQANRTRVA 155

Qy     118 RYTYNKSTDTLEKPVDLLAGLPSSKDHDSGRLVIGPDQKIYYTIGDQGRN--QLAYLFLP 175
      | : : | : : : | | | | : : : | | | | : | : | :
Db     156 RAVFDGEKLTDWQVIFEVGQTKPGGQFFGSRLTWLPDETLLVSI GDGGNPPVELEGDFIR 215

Qy     176 NQAQHTPTQQELNGKDYHTYMGKVLRLNLDGSIPKDNPSFNG--VVSHIYTLGHRNPQGL 233
      ||| : : : | : : | | : : | | | | : : | | | | | |
Db     216 QQAQNRA-----SHLGKIIIRINDDGTVPADNPFRRNDPKAAPEVWSYGHRNIQGL 264

Qy     234 AFTP-NGKLLQSEQGPNSDDEINLIVKGGNYGWPVNAVAGYKDDSGYAYANYSAANKSIKD 292
      | : | : : | | | | | | | | | | | : | : | : | : | : | : | :
Db     265 AYDPVTQKVWATEHGSRGGDELNLIQKGKNYGWPVVSFSKE-----YSTDQPVA----- 313

Qy     293 LAQNGVKVAAGVPVTKESEWTGKNFVPLKTLTYTVQDTYNYNDPTCGEMTYICWPTVAPS 352
      | | : | | | : | : | : | : | : | : | : | : | : | : | : | :
Db     314 -----PATSRPD-----MVDPLQ-----IWTPTAAPS 335

Qy     353 SAYVYKGGKKAITGWENTLLVPSLKRGVIFRIKLDPTYSTTYDDAVPMFKSNNRYRDVIA 412
      : | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db     336 GLTIYNGDRH--PEWQGTIFAGGLVDRGIRHLRLDENNQIIDETTISI---GQVRDVRQ 390

Qy     413 SPDGNVLYVLTDTAGNVQKDDGSVTNTLENPGSLIK 448
      ||| : | | | | : | | | : | : | : | : | : | : | : | : | : | :
Db     391 GPDGHV-YVLT-----QNGQLLR 409

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